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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

THE VICTOR CHANG CARDIAC

RESEARCH INSTITUTE, THE

GENERAL HOSPITAL CORPORATION and

THE WALTER AND ELIZA HALL

INSTITUTE OF MEDICAL RESEARCH.

(ii) TITLE OF INVENTION:

NOVEL THERAPEUTIC MOLECULES

AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIES COLLISON CAVE

(B) STREET: I LITTLE COLLINS STREET

(C) CITY: MELBOURNE

(D) STATE: VICTORIA

(E) COUNTRY: AUSTRALIA

(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: INTERNATIONAL APPLICATION
- (B) FILING DATE: 26-MAR-1999
- (C) CLASSIFICATION:

(vii) PREVIOUS APPLICATION DATA:

- (A) APPLICATION NUMBER: PP2634/98
- (B) FILING DATE: 27-MAR-1998

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: HUGHES, DR E JOHN L
- (C) REFERENCE/DOCKET NUMBER: EJH/TDO/DK

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: +61 3 9254 2777
- (B) TELEFAX: +61 3 9254 2770
- (C) TELEX: AA 31787

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(2)	INFORMATION	FOR SI	EO ID	NO:1:
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- SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear (i)
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 199..453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGCTAAGACC TTGTGAAT ATG TCG AAG CAG CCA ATT TCC AAC GTC AGA GCC Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala 1	GAA?	TTGA	GAT	cccc	GCTC	AG A	GGAC	ACCG(G GA	GTTC	CTTC	TAT	CCTG	TAA	AGCG	CITITT	120
Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala 10 ATC CAG GCG AAT ATC AAT ATT CCA ATG GGA GCC TTT CGT CCG GGA GCT Ile Gln Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala 20 20 20 20 20 20 20 20 20 2	GTGT	rrr	TGC	ACCT	GGCC	sc c	TGGG	ACTG'	r cc	rcag(GCAG	TAA	ACCA	ATC	CAGA	GAGCAG	180
Ile Gln Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala 15 20 32 25 32 32 32 32 32 32 32 32 32 32 32 32 32	GGCT	raag.	ACC	TTGT	GAAT					Pro					Arg		231
Gly Gln Pro Pro Arg Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly 30 GCT CCT ACC ACC TCA GAG GAA AAG AAG CCA ATT CCT GGA ATG AAG AAA Ala Pro Thr Thr Ser Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys 45 TTT CCA GGA CCT GTT GTC AAC TTG TCT GAG ATC CAA AAT GTT AAA AGT Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser 60 GAA CTG AAA TTT GTC CCC AAA GGT GAA CAG TAGTCGAAAG GACACAAAAG Glu Leu Lys Phe Val Pro Lys Gly Glu Gln 80 TTCACATTGG ATGCTTAGAA TCAGGAGATG CATTTCGTTG ACGTGTTTTT CCAAGGGAGA AAAAACAATG GGTTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA 59: CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTTGTACAT TTATATTTCT TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 71: CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA				Asn					Met					Pro			279
Ala Pro Thr Thr Ser Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys 50 TTT CCA GGA CCT GTT GTC AAC TTG TCT GAG ATC CAA AAT GTT AAA AGT Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser 60 GAA CTG AAA TTT GTC CCC AAA GGT GAA CAG TAGTCGAAAG GACACAAAAG Glu Leu Lys Phe Val Pro Lys Gly Glu Gln 80 TTCACATTGG ATGCTTAGAA TCAGGAGATG CATTTCGTTG ACGTGTTTTT CCAAGGGAGA AAAAACAATG GGTTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTTGTACAT TTATATTTCT TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77			Pro					Glu					Thr				327
Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser 60 65 70 75 GAA CTG AAA TTT GTC CCC AAA GGT GAA CAG TAGTCGAAAG GACACAAAAG Glu Leu Lys Phe Val Pro Lys Gly Glu Gln 80 85 TTCACATTGG ATGCTTAGAA TCAGGAGATG CATTTCGTTG ACGTGTTTTT CCAAGGGAGA 53: AAAAACAATG GGTTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA 59: CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTTGTACAT TTATATTTCT 65: TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 71: CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77		Pro					Glu					Pro					375
Glu Leu Lys Phe Val Pro Lys Gly Glu Gln 80 85 TTCACATTGG ATGCTTAGAA TCAGGAGATG CATTTCGTTG ACGTGTTTTT CCAAGGGAGA 53. AAAAACAATG GGTTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA 59. CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTTGTACAT TTATATTTCT 65. TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 71. CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77	Phe					Val					Ile					Ser	423
AAAAACAATG GGTTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA 59: CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTTGTACAT TTATATTTCT 65: TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 71: CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77					Val					Gln	TAGI	rcgaa	AG (SAÇA(CAAAA	AG.	473
CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTTGTACAT TTATATTTCT 65: TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 71: CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77	TTCA	CATI	rgg i	ATGC	rtaga	LA TO	CAGGA	GATO	CAT	TTCC	TTG	ACGT	GTT	rtt (CCAAC	GGAGA	533
TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT 71. CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77	AAAA	ACAA	TG (GGTTC	GAAAT	A A	ACAA(TTC	TGA	ACAI	TTT	ATAC	ATT	rgt i	atgai	GATCA	593
CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTTATGAA 77	CAAA	.ccT	CT (GAATO	CCC	LA GI	ACTCI	CAGCA	AAA	ATAT	CCT	GTTI	GTA	CAT '	TTAT!	TTTCT	653
	TÇCT	TITA	CT '	TGGT1	rgca?	T T	TCAC	TTTA	GCI	'ACA1	TTT	TGGC	ACC.	rtg '	TAGAC	CAAAT	713
cccc	CAGO	ACAC	GA A	ATTTA	CAAC	C TO	GGAA	GTG1	GGI	TTTC	AGG	AGAC	ATG:	rga '	rttt	TATGAA	773
	GGGG	G															778

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(2) INFORMATION FOR SE	EQ ID	NO:2:
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- SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Arg

Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly Ala Pro Thr Thr Ser

Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys Pne Pro Gly Pro Val

Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser Glu Leu Lys Phe Val 65

Pro Lys Gly Glu Gln

(2) INFORMATION FOR SEQ ID NO: 3:

- SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 887 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 185..448
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AGATCGCAGC TCAGAGGACA CCGGGCGCCC CTTCCACCTT CCAAGGAGCT TTGTATTCTT	120
GCATCTGGCT GCCTGGGACT TCCCTTAGGC AGTAAACAAA TACATAAAGC AGGGATAAGA	180
CTGC ATG AAT ATG TCG AAA CAG CCA GTT TCC AAT GTT AGA GCC ATC CAG Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala 11e Gln 1 5 10 15	229
GCA AAT ATC AAT ATT CCA ATG GGA GCC TTT CGG CCA GGA GCA GGT CAA Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln 20 25 30	277
CCC CCC AGA AGA AAA GAA TGT ACT CCT GAA GTG GAG GAG GGT GTT CCT Pro Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro 35 40 45	325

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Pro Thr Se	CG GAT GAG (er Asp Glu (50	AG AAG AAG Slu Lys Lys 55	Pro Ile Pro	A GGA GCG AAG AAA CTT O Gly Ala Lys Lys Leu 60	37
CCA GGA CC Pro Gly Pr 65	T GCA GTC A TO Ala Val A	AT CTA TCG sn Leu Ser 70	GAA ATC CAG Glu Ile Gln	AAT ATT AAA AGT GAA Asn Ile Lys Ser Glu 75	42]
	r Val Pro L			AAG AAAAAAGGAT	468
TGATGTGAAG	AAATAAAGAG	GCAGAAGATG	GATTCAATAG	CTCACTAAAA TTTTATATAT	528
TTGTATGATG	ATTGTGAACC	TCCTGAATGC	CTGAGACTCT	AGCAGAAATG GCCTGTTTGT	588
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CTCACAGAAC	AAATTAGCCC	ATAAATTCAA	CACCTGGAGG	GTGTGGTTTT GAGGAGGGAT	708
atgat tt tat	GGAGAATGAT	ATGGCAATGT	GCCTAACGAT	TTTGATGAAA AGTTTCCCAA	765
CTACTTCCT	ACAGTATTT	GGTCAATATT	TGGAATGCGT	TTTAGTTCTT CACCTTTTAA	828
ATTATGTCAC	TAAACTITGT	ATGAGTTCAA	TTTATAATA	GACTAAATGT AAAATGTGA	887

- (2) INFORMATION FOR SEQ ID NO:4:
 - SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 88 amino acids

 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro

Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro Pro

Thr Ser Asp Glu Glu Lys Lys Pro Ile Pro Gly Ala Lys Lys Leu Pro

Giy Pro Ala Val Asn Leu Ser Glu Ile Gln Asn Ile Lys Ser Glu Leu

Lys Tyr Val Pro Lys Ala Glu Glm 85

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- SEQUENCE CHARACTERISTICS: (i)
 - (A) LENGTH: 75 amino acids (B) TYPE: amino acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ser Lys Gln Pro Ala Ser Asn Ile Arg Ser Ile Gln Ala Asn Ile

Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Lys

Arg Lys Glu Phe Ser Thr Glu Glu Glu Gln His Vel Pro Thr Pro Glu

Ser Glu Glu Lys Ser Glu Glu Lys Lys Pro Ile Pro Gly Ala Val Lys

Leu Pro Gly Pro Ala Phe Asn Leu Ser Glu Thr 70

(2) INFORMATION FOR SEQ ID NO:6:

- SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 887 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- SEQUENCE DESCRIPTION: SEQ ID NO:6: (xi)

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 887 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- SEQUENCE DESCRIPTION: SEQ ID NO:7: (xi)

GGATAAGACT GCATGAATAT GTCGAAACAG CCAGTTTCCA ATGTTAGAGC CATCCAG

(2) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 887 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
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AAAGAATGTA CTCCTGAAGT GGAGGAG	87
(2) INFORMATION FOR SEQ ID NO:9:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 887 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
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GGACCTGCAG TCAATCTATC GGAAATCCAG AATATTAAAA GTGAACTAAA ATATGTCCCC	120
AAAGCTGAAC AGTAGTAGGA AGAAAAAG	149
(2) INFORMATION FOR SEQ ID NO:10:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 887 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
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CACCTCACAG AACAAATTAG CCCATAAATT CAACACCTGG AGGGTGTGGT TTTGAGGAGG	240
GATATGATTT TATGGAGAAT GATATGGCAA TGTGCCTAAC GATTTTGATG AAAAGTTTCC	300
CAAGCTACTT CCTACAGTAT TTTGGTCAAT ATTTGGAATG CGTTTTAGTT CTTCACCTTT	360
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SEQUENCE LISTING

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atc ca				aat				gga					gga		279
ggg ca	ng cct n Pro 30	ccc Pro	aga Arg	agg Arg	aaa Lys	gag Glu 35	agt Ser	act Thr	cct Pro	gaa Glu	act Thr 40	gag Glu	gag Glu	gga Gly	327
gct co															375

ttt cca gga cct gtt gtc aac ttg tct gag atc caa aat gtt aaa agt

423

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Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser 60 65 70 75	
gaa ctg aaa ttt gtc ccc aaa ggt gaa cag tagtcgaaag gacacaaaag Glu Leu Lys Phe Val Pro Lys Gly Glu Gln . 80 85	473
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Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys Phe Pro Gly Pro Val	
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Gly 65		Ala	Val	Asn	Leu 70		Glu	Ile	Gln	Asn 75		Lys	Ser	Glu	Leu 80	
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		35					40					45		Pro		
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Pro Trp Met Lys Leu Phe Phe Lys Ile Lys Pro Leu Leu Lys Ser Ala
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Glu Thr Glu Lys Glu Met Ala Thr
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Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro
Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp Ser Leu Pro Phe
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Val Gly Glu Lys Arg Val Thr Glu
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<223> consensus sequence
<221> VARIANT
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<400> 15
Ile Gln Xaa Xaa Ile Arg
<210> 16
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<213> Homo sapiens
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Ser Glu Glu Asp Gly Phe Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu
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Ser Val Leu Arg Glu Glu Ser Glu Ser Val
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Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg
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Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu
<210> 18
<211> 24
<212> PRT
<213> Homo sapiens
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Gln Ile Leu Trp Phe Arg Gly Leu Asn Arg Ile Gln Thr Gln Ile Arg
                                    10
Val Val Asn Ala Phe Arg Ser Ser
            20
<210> 19
<211> 20
<212> PRT
<213> Homo sapiens
<400> 19
Ala Arg Arg Lys Leu Lys Ala Ala Val Lys Ala Val Val Ala Ser Ser
Arg Leu Gly Ser
<210> 20
<211> 26
<212> PRT
<213> Apis mellifera
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<400> 20
Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu 1 5 10 15
Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln 25